MoP302 The spectrum of infectious diseases attended at the emergency ward of an urban general hospital

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Objectives: The infectious pathology and the antibiotic prescription to patients in the emergency ward were studied.
Methods: We revised the clinical records of all patients discharged during October 1999 from the general emergency ward of an urban teaching hospital, coveting a population of 500,000. Statistical analysis was performed with Stat View Statistical package.
Results: A total of 6,295 emergencies were attended during this month and a total of 5,470 (87%) were discharged. Infectious disease was diagnosed in 648/5,470 (11.84%). Mean age was 50.3 ± 23.0 years (18–97). 321 (49.54%) were males. The 5 most frequent presenting symptoms were: dyspnea 72 (11.11%), trunk and limb pain 62 (9.57%), abdominal pain 60 (9.26%), cough 52 (8.03%) and otalgia 50 (7.72%). Fever was present in 209 (32.2%). Complementary examinations were: chest x ray 231 (35.65%), blood analysis 205 (31.63%), urine analysis 91 (14.09%), blood arterial gas 57 (8.79%), and blood culture 29 (4.52%). Microbiological data was obtained in 12 (1.85%) cases. The most frequent diagnoses were: lower respiratory tract infection 127 (19.59%), skin and soft tissue infection 104 (16.04%), upper respiratory tract infection 99 (15.27%), acute gastroenteritis 84 (12.96%), and urinary infection in 57 (8.8%). 463 of the patients required antibiotic treatment: amoxicillyne-clavulanate 261 (54.21%), quinolones 86 (18.50%), macrolides 40 (8.6%), cloxacilline 36 (7.7%), cephalosporins 12 (2.5%).
Conclusions: Infectious diseases are very frequent pathology in the emergency ward. Dyspnea is the most frequent symptom, and bronchial and pulmonary pathology are the most prevalent entities observed. Microbiological diagnoses is rare. Amoxicillyne-clavulanate is the most frequently prescribed antibiotic.

MoP303 The etiologic spectrum of bacteriemia seen in a hematology unit

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Objectives: All episodes of bacteriemia and fungemia occurring among patients with high risk of severe sepsis observed in the Department of Hematology University Hospital in Cracow were analysed with regard to trends in causative organisms from 1993 to 1999. Three hundred and eleven patients with various degrees of immunosuppression, were retrospectively estimated in relation to the frequency of the blood-stream infections especially caused by new nosocomial pathogens.
Methods: A total number of 1328 blood cultures were tested using the automated-calorimetric BacT/Alert microbial detection system based on continuous-monitoring technology (Organon Teknika Corporation). The strains were identified in automatic ATB system using commercial strips with biochemical tests (bio-Merieux).
Results: Gram(+) and Gram(−) bacteria accounted for 53.9% and 34.4% of the episodes, respectively. There was a high incidence of invasive fungal infections-11.7%. The upward trend in Gram(+) bacteriemia appeared to be related to a significant increase in both *Enterococci* (0.0 to 6.4%) and *Viridans group Streptococci* (mainly *S. mitis*) (0.0 to 3.7%) respectively to the years. New groups of non-fermentative bacilli such as *Stenotrophomonas maltophilia* showed a tendency to increase and ranged from 3.7 to 11.9% during the past two years. Between 1993 and 1999 *Candida albicans* fungemias were not reported at all. A shift higher isolation of non-Candida spp. was observed. Two cases of fungemia caused by *Trichosporon beigelii* and *T. asahii* were described in 1998–1999. The proportion of poly versus monomicrobial infection has became changed from 25.0% vs 75.0% in 1996–1997 to more than 48.0% vs 51.2% in 1999.
Conclusions: Constant analysis of microbial evolution and localisation of infections should be essential element in control of hospital infections program.

MoP304 Prevalence of hepatitis C virus in pregnancy

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Objective: To assess the prevalence of anti-HCV and identify the risk factors for HCV infection in pregnant women.
Methods: 5.120 consecutive pregnant women attending the "Helena Venizelou" Maternity Hospital were screened for HCV antibodies by ELISA-2 (Abbott) and RIBA-2 (Innogenetics) methods. All women were interviewed to select relevant epidemiological data.
Results: The overall anti-HCV prevalence in pregnant women was 0.66% (34/5.120). The prevalence for Greek women was 0.61% (24/3.930) and for immigrants 0.84% (10/1.190). Risk factors for HCV infection were identified in 10 of the 34 anti-HCV positive women: a) 4 (11.8%) had been blood transfused, b) 4 (11.8%) were intravenous drug users, c) 2 (5.9%) were health care workers.
Conclusions: The prevalence of HCV infection is relatively low in Greek pregnant women but is higher in immigrants. The known risk factors were identified in only 29.4% for the anti-HCV(+) women.

MoP305 The results of a third-year period urine cultures in a Greek hospital

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Objective: The purpose of this study is to present our results from a third-year period urine cultures in our hospital.
Materials and Methods: During a 3-year period from 1997 to 1999 18.280 urine specimens were examined for bacterial pathogens in the microbiology laboratory at Hippokration General Hospital of Athens. Urine cultures and identification of bacterial pathogens were performed by standard microbiological methods. Antimicrobial susceptibility tests were performed by the agar diffusion method advocated by NCCLS.
Results: A 10% of the urine cultures were positive. There 1816 strains were isolated. The most frequently isolated pathogens were the Gram negative bacteria E. coli (60%), Klebsiella spp (19%), Proteus spp (7%), Pseudomonas spp (10%) and the gram positive cocci Enterococcus spp (11%) and Staphylococcus aureus (0.6%). As regards the sensitivity of the bacteria isolated, it is worth nothing that: four strains of enterococci spp were resistant to vancomycin and there is an increasing rate of resistance of enterococci against quinolones. There was a decreasing rate of resistance of gram negative bacteria against Ampicillin and Ampicillin-Clavulanic acid, while the resistance to cephalosporins remained at the same level.
Conclusion: It is of great importance to be a close cooperation between the committee of nosocomial infections and the clinicians in order to reduce the resistance to antibiotics.

P:14/3 – Surveillance of infectious diseases and antibiotic resistance - III

MoP306 Prevalence of macrolide - and aminoglycoside resistance genes in European *Staphylococcus aureus* isolates

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Objectives: To study the prevalence of macrolide and aminoglycoside resistance genes in *Staphylococcus aureus* isolates derived from 24 European university hospitals.
Methods: The prevalence of the macrolide resistance genes (*ermA, ermB, ermC, msrA/msrB, ereA, ereB*) and of the aminoglycoside resistance genes (*aac(6')-Ie + aph(2'')*, *ant(4')-Ia*, *aph(3')-IIIa*) was studied by PCR in 851 clinical erythromycin-resistant and 551 aminoglycoside-resistant *S. aureus* isolates, respectively.
Results: The *ermA* gene was more common in methicillin-resistant *S. aureus* (MRSA) (88%), mainly in strains with a constitutive MLSB expression, than in methicillin-susceptible *S. aureus* (MSSA) (38%), whereas *ermC* was predominant in MSSA (47%), mainly in strains with an inducible expression, and less so in MRSA (5%). The *ereB* gene was only found in MRSA (1%), while *ereA* was not detected. The *msrA/msrB* gene was only detectable

in MSSA (13%). Amongst isolates of *S. aureus* the most prevalent aminoglycoside resistance gene was *aac(6')-Ie + aph(2")*, found in 79% of MRSA and 47% of MSSA. The least common was *aph(3')-IIIa*, occurring in 5% of MRSA and 17% of MSSA.
Conclusion: Resistance to erythromycin in European *S. aureus* isolates is mainly due to the presence of *ermA* and *ermC* genes, while *aac(6')-Ie + aph(2")* is the most common aminoglycoside resistance gene.

MoP307 Epidemioiogy of varicella in Slovenia (from 1979 to 1998)

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Objectives: The epidemiologic characteristics of reported varicella cases over a period of the last twenty years were analysed.
Methods: In Slovenia, varicella is a notifiable communicable disease which must be reported. The registration form requires the following data: full name, age, date of onset of the disease. Since 1990, data have been collected on whether the child attended a day-care facility and whether he/she was hospitalised due to varicella. Data collected from 1979 to 1998 are presented.
Results: The annual incidence rate of varicella cases ranged from 11 086 (in 1994) to a maximum of 21 141 (in 1987). The average incidence for the twenty-year period was 815.2/100000 (minimum 557.2 and maximum 1058 per 100000) inhabitants. In the total number of reported cases, on average, 50.2% of cases were male and 49.8% female. The greatest number of varicella cases was established among children up to 6 years of age (pre-school children), who accounted for 52–78% of all reported cases. The greatest changes were observed in the age group from 1 to 2 years. In 1979, only 4.25% of reported varicella cases belonged to this age group, while in 1998 there were as many as 17.13%. The number of reported cases among primary school children (children aged between 7 and 14) as well as among adolescents aged between 15 and 19 decreased steadily over the observed period. The percentage of varicella cases in persons older than 20 was low, but an increase in incidence may be noticed in the 20–29 year age group. Each year varicella cases peaked in the months of December and January, while the lowest incidence rates were found in July and August.
Conclusion: The epidemiology of varicella in Slovenia is based merely on passively reported cases, therefore the recorded incidence is undoubtedly lower than it would have been, had there been active supervision. In spite of this, the following observed changes can be noticed: the increased incidence of varicella in very small children and in young adults. The epidemiologic changes concerning varicella will need to be taken into account when planning possible vaccination programmes against varicella.

MoP308 Comparison of serotyping, antibiotyping and plasmid profile analysis for the epidemiological investigation of *Salmonella*

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Objective: To investigate the serotypes, antibiotypes and plasmid profiles of *Salmonellae* isolates with three different epidemiological specifications and to assess the efficiency of each method for the epidemiological analysis in this genus.
Methods: A total of 71 *Salmonellae* isolates were taken into the study. Of these, 46 were isolated from two nosocomial outbreaks which occured in different settings and time intervals (groups 1 and 2). Twenty-five were from sporadic cases seen at a university hospital in 1995 (group 3). Serotypes were determined by antisera against Salmonella O and H antigens. Antibiotypes were determined by testing in vitro susceptibility to 29 antibiotics. Plasmid DNA was prepared by the method of Kado and Liu.
Results: The first group included 24 Salmonella strains isolated from neonatal and premature infants at Tepecik Social Security Hospital in 1995. In this group, 91.6% of the isolates were identified as *S. typhimurium* and 8.4% as *S. enteritidis*. A total of 11 antibiotypes were found, eight of which were only detected in this group of isolates. The second group consisted of 22 strains isolated at Behçet Uz Children's Hospital in 1993. All of the isolates within this group belonged to typhimurium serotype and 10 antibiotypes different from the other groups, were detected. The third group consisted of 25 salmonellae isolated from sporadic cases at Dokuz Eylul University Hospital in 1995. Six different serotypes were found within this group. These strains possessed 11 antibiotypes. Although specific plasmid patterns were found in each group, plasmids with molecular sizes of 210, 13 and 10 kb were common in all three groups. In addition, outbreak isolates possessed common 2.5 and 2.0 kb plasmids. On the other hand plasmids with molecular sizes of 60 kb, 45 kb and 110 kb, seemed to be specific for the first, second and third groups respectively.
Conclusion: Serotyping is only useful as an epidemiological marker when an outbreak is caused by an unusual serotype. When common serotypes were isolated as in our case, antibiotypes combined with specific plasmid profiles can be used as epidemiological markers not only for outbreaks but also for sporadic cases.

MoP309 Relationship between *Salmonella* serotypes and age of patient

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Objective: To evaluate a possible correlation between *Salmonella* serotypes and patients' age, retrospectively.
Methods and Results: A total of 71 *Salmonella* strains with 3 different epidemiologic specifications were taken into the study. Of the patients from whom the strains were isolated, 48 (67%) were 0–2 years old, 5 (7.0%) were 2–10 years old and 18 (25.4%) were older than 10 years. The most common serotype in these age groups were *S. typhimurium* (91.6%), *S. typhi* (40%) and *S. typhi* (50%), respectively. When the distribution of the serotypes according to patient's average age was analyzed, the patients from whom *S. typhimurium* was isolated from had the lowest age average (13 months) and for the patients from whom *S. typhi* was isolated the average age when the infections had been detected, was 23 years. In this study 67.6% of the cases consisted of premature and infants (ages between 0–2 years) in whom *S. typhimurium* was the most common serotype (91.6%). Fifteen percent of all strains was *S. typhi* which had been isolated from the oldest child and adults.
Conclusion: These findings are particularly important for empiric antibiotic treatment according to age groups in *Salmonellae* infections because antibiotic susceptibilities also differ according to the serotypes.

MoP310 Epidemiological analysis by molecular techniques of ESBL(+) *Klebsiella pneumoniae* clinical isolates

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Objectives: *Klebsiella pneumoniae* strains producing extended-spectrum beta-lactamases (ESBL) have been recognized as an important cause of hospital-acquired infections. The identification of the source of infection and ways of transmission are important for the infection control. The aim of this study was to differentiate *K. pneumoniae* ESBL(+) clinical isolates from one another by means of two different molecular techniques.
Methods: We studied twenty nine ESBL(+) *K. pneumoniae* clinical isolates recovered from patients in the Intensive Care Unit (ICU) of our hospital within a short period of time (Mars 1999–July 1999). Routine antibiotic susceptibility tests and ESBL detection were performed on the Vitek automated system (bioMérieux). The epidemiological analysis of the strains was made by two molecular methods: 1) plasmid analysis and 2) random amplified polymorphic DNA (RAPD) analysis. With the first method, plasmid DNA from *K. pneumoniae* isolates was extracted using the QIAGEN columns according to the manufacturer's instructions and analyzed, without digestion, by 0.8% agarose gel electrophoresis. With the second method, *K. pneumoniae* DNA was extracted by using Chelex anion exchange resin (Perkin Elmer) and analyzed by using three arbitrary chosen primers.
Results: Plasmid analysis gave 4 different profiles. RAPD analysis with the three arbitrary primers gave 10 different profiles. When plasmid and RAPD results were compared, we found that seven isolates shared the same plasmid and RAPD patterns.
Conclusions: Plasmid and RAPD analysis were proven useful and powerful epidemiological tools for the identification of nosocomial transmission of ESBL(+) *K. pneumoniae* clinical isolates.

MoP311 Advanced interactive epidemiology reports utilizing the BD Phoenix® EpiCenter® system

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Objective: Determine if modern data visualization components and data integrity rules can be integrated into an effective epidemiology data mining tool for use with the new BD Phoenix® Data Management platform. (EpiCenter®, BD Biosciences, Sparks, MD USA)
Methods: EpiCenter, a microbiology data management system for the new BD Phoenix automated microbiology system was developed that integrates state-of-the-art software components, an expert system, and data validation logic. This system was designed to overcome several common problems in interpreting microbiology test data. First, complete and accurate representations of microbiology results were designed into the schema of the database. Second, validation rules along with an expert system were built on top of the database to insure accuracy of the data being saved. Third, modern graphical user interface tools and techniques were combined to enable the data to be easily examined in a variety of ways. Finally, a sophisticated set of predefined queries and reports were generated to provide useful tools to examine historical microbiologic data.
Results: 100+ predefined queries and 15+ predefined reports were developed to cover traditional epidemiology data tracking. These queries and reports included MIC trending, isolates with similar resistance patterns, multiply resistant isolates, isolates with resistance mechanisms, percent susceptible and organism incidence reports. The data is bundled in a flexible, dynamic, reporting format that allows the user to examine the data at a high level, or drill into detailed information on a specific isolate.
Conclusions: The BD Phoenix® EpiCenter® System provides a useful tool track epidemiology of infectious diseases.

MoP312 Association between bacterial vaginosis and preterm delivery

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Objectives: To investigate the relationship of Bacterial vaginosis with preterm birth (< 37 wks).
Methods: Five hundred and twenty seven (527) singleton women at 22^{+5}–24^{+6} wks of gestation were screened for *Gardnerella vaginalis* colonization of the lower genital tract. Cultures were performed from cervical and high vaginal swabs.
Results: Fifty seven women (10.8%) delivered at less than 37 completed wks of gestation. The prevalence of *Gardnerella vaginalis* as assessed by Gram stain and culture of vaginal smears was 9.3% (49/527). Ten of the pregnant women colonized with *Gardnerella* vaginalis delivered preterm (20.4%). The incidence of preterm delivery was significantly increased in women with *Gardnerella vaginalis* colonization (relation risk, RR = 2.08).
Conclusions: Those results show that *Gardnerella vaginalis* colonization of the lower genital tract is strongly associated with an increased risk of preterm delivery.

MoP313 Antibiotic resistance in non-typhoidal Salmonellae during an eight year period (1990–1997)

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Objectives: The aim of this study was to investigate the evolution of resistance to antibiotics of a representative sample of various non-typhoidal salmonella serotypes, from human, animal, food and environmental sources.
Material and methods: The Resistance Rates (RRs) of 1548 Salmonella isolates to 15 antibiotics were determined by using the MICs broth microdilution automated method, as outlined by the NCCLS. The isolates have been randomly selected from the countrywide collection of National Reference Centre of Salmonella and Shigella. The material was divided in 3 groups: group A consisted of 709 *S. enteritidis* isolates, group B of 363 *S. typhimurium* ones and group C of 476 isolates of various serotypes.
Results: The RRs, between 1990 and 1997, for group A ranged from 31 to 33%, in ampicillin (peak 1994: 64%) and from 6 to 18% in tetracycline (peak 1996: 24%); in group B the RRs to ampicillin and tetracycline were respectively 19–38% (peak 1996: 42%) and 18–61% (peak) and in chloramphenicol 9–31% (peak 1996: 39%). In 1996, the RRs to almost all antibiotics declined for *S. enteritidis* and in 1997 there was a sharper decrease. The group C isolates were overall more susceptible than those of A and B groups. The RRs were higher in non-human isolates compared to the human ones in group A; on the contrary, the human isolates were more resistant in B and C groups. Group A has proved to be the most resistant group, while group B the most multiresistant one.
Conclusions: The RRs in *S. enteritidis*, especially to ampicillin were higher than those observed in other countries. The great proportion of multiresistant isolates in *S. typhimurium* is cause of concern.

MoP314 Nasopharyngeal colonization with *Streptococcus pneumoniae* in the elderly: Prevalence, risk factors and dynamics

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Objective: To determine the prevalence, risk factors and dynamics of nasopharngeal colonization with *Streptococcus pneumoniae (S. pne)* in the elderly.
Methods: A nasopharyngeal swab (NPS) was directly plated on a blood agar containing polymyxin B and incubated at 35° C and 5% CO2 for 48 hours. A second NPS was cultured after preincubation in Todd-Hewitt broth. 21 nursing home residents (7 *S. pne* positive and 14 *S. pne* negative) were screened 5 times within 3 months to establish the dynamics of nasopharyngeal colonization.
Results: The prevalence of nasopharyngeal colonization with *S. pne* was 6.3% (13/206). Direct plating yielded 9 carriers and preincubation in Todd-Hewitt broth 4 additional cases. The colonization rate of 109 community dwelling elderly and 97 nursing home residents was 5.5% and 7.2%, respectively (NS). No significant difference in risk factors was observed between colonized and non-colonized subjects. Colonized subjects tended to be male (M/F ratio 1.2 vs. 0.5 p:0.23), to have a prior hospitalization (46.1% vs. 22.3% p:0.08), to be smokers (23% vs. 10.8% p:0.18) and to be vaccinated against influenza (84% vs. 62%, p:0.14). Of 7 *S. pne* positive nursing home residents 2 showed permanent colonization, 3 intermittent colonization and 2 became negative. Of 14 *S. pne* negative nursing home residents 7 stayed negative, 7 showed intermittent colonization and 1 permanent colonization after 3 months follow-up.
Conclusions: The prevalence of nasopharyngeal colonization with *S. pne* in elderly subjects is low. Transient colonization, however, occurs in 50% of nursing home residents within a 3 month period.

MoP315 Infection management at three intensive care units

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Objectives: We have retrospectively analysed the infection management of three ICU (medicine MICU, surgery SICU, anaesthesiology AICU) of a large teaching hospital according to various parameters.
Methods: During a 24 months period (I/98 to XII/99) we followed the antimicrobial usage, the number of clinical specimens submitted for microbiological work-up and the kind and resistance of bacterial isolates. Some of the results are summarised in the following table.
Results

	MICU	SICU	AICU
No. of admissions	1566	1265	2526
Average length of stay (days)	4.89	5.98	1.49
Average no. of microbiol. Specimens/patient	8.27	2.67	1.18
No. of specimens	12948	3384	2980
Per cent positivity	11.14	4.4	7.16
Treatment days/patient			
Ceftazidime	0.58	0.39	0.125
Piperacillin/tazobactam	0.66	0.68	0.0068
Imipenem	0.45	0.94	0.22
Ciprofloxacin	0.34	0.22	0.0028

Conclusions: The MICU submitted significantly more specimens/patient than other ICUs. The spectrum of pathogens isolated and the antibiotic use was different for each ICU. This seemed to have no significant impact on resistant rates of various species.

MoP316 Antimicrobial resistance of group A Streptococci: A 7-year follow-up study

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Objectives: To determine the resistance rates of group A Streptococci (GABHS) to commonly used antimicrobial agents for the treatment of pharyngitis in children.
Methods: A total of 1,074 GABHS obtained from throat swabs of children with pharyngitis from January 1993 through December 1999, were evaluated. The antimicrobial susceptibility testing was performed by the Kirby-Bauer diffusion disc method. In addition, the MIC values of erythromycin and clindamycin in resistant to erythromycin strains isolated from January 1996-December 1999 were determined by the E test, while the resistance phenotype of these isolates were characterized by the double-disc induction test.
Results: Resistance to erythromycin were detected in 181 strains (16.9%) and to clindamycin in 7 (1.2%). None of the 1,074 GABHS strains were resistant to penicillin, cefactor, cefprozil and cefuroxime. The resistance rates of GABHS to erythromycin through the study period were as follows: 1993, 7.1%; 1994, 9.1%; 1995, 12.9%; 1996, 19.8%; 1997, 222.7%; 1998, 23.8%; 1999, 23.5%. Of these strains (41.8%) had the inducible MLS phenotype, 5.2% the constitutive MLS phenotype and 53.0% the M phenotype. The highest MICs levels of erythromycin (MIC90 = 24 mg/ml) were exhibited by the strains with M-phenotype, while similar MIC values of clindamycin (MIC90 = 0.25 μg/ml) were observed between the two main resistance phenotypes.
Conclusions: The increasing frequency of erythromycin resistance and the high prevalence rates of inducible MLS resistance phenotype in GABHS should be taken into account for the treatment of pharyngitis.

MoP317 *Toxoplasma gondii* in pregnant women: Seroprevalence, incidence and its evolution in an area of Madrid

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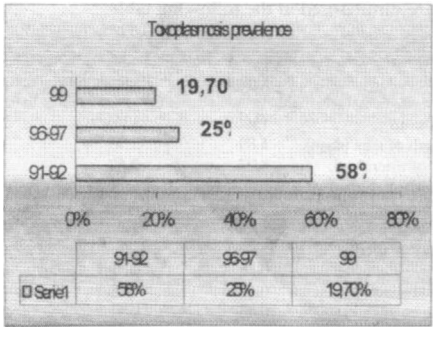
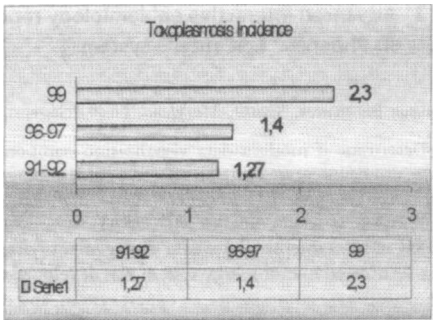
Objectives: To know the situation of *T. gonadii* infection in pregnant women in our area during the last year (1999), and analyze the evolution of seroprevalence and incidence in the last decade.
Method: We studied 1593 pregnant women who was attended in our area (La Paz Hospital, Madrid) during 1999. Specific IgG antibody to *Toxoplasma gondii* was detected by means of E.L.I.S.A. (Wampole Laboratories®). All woman with IgG antitoxoplasma positive was considered immune. Serological evidence of primary *T. gondii* infection was defined as seroconversion during pregnancy, presence of specific IgM and low avidity IgG.
Results: The seroprevalence was 19.77% during this year. The incidence of primary infection was stimated to be 2.3 ml per year (3/1278).





Conclusions: • The data of 1999 show a decrease in prevalence as compared to previous data from the same area, so the risk of primary infection is enhanced.
• It is important to emphasize the importance of prevention in no-immune pregnant women.

MoP318 Pediatric leishmaniasis: Epidemiologic and diagnosis

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Objetives: To analyze the epidemiologic features of pediatric leishmaniasis in our hospital.
Methods: From January 1.992 to December 1.999, 162 child with clinic suspicion of leishmaniasis visceral were studied. Specific serology by IFI (Leishmania-Spot IF, bio Merieux.s.a.) and direct microscopic examination of the bone marrow was effected. Titers of 1/80 are said to be suspect levels.
Results: 21 cases (15.4%) had positive direct microscopic examination and IFI. Titers ranged between 1/80 and 1/2560. Two cases had positive skin biopsy.

Of all 21 patiens 33.3% had dogs, 76.2% lived in rural area/outskirts. All of them had fever, pancytopenia and hepatosplenomegaly and 38.1% had also adenopathies.

Age distribution was: <1 year (24%), 1–2 years (57%) and > 2 years (19%).
Conclusions: The major incidence of the disease was observed in autum and winter, because of the vector life cycle. Although dogs are the main reservoir; the microclimate asociated with the outskirts, and river banks seem to be other important factor.

MoP319 Incidence of *Listeria monocytogenes* infection

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Introduction: *L. monocytogenes* is the only human pathogen among the seven species of this genus. The annual incidence of listeriosis has been estimated to be 0.2 cases per 100000 in several European countries.
Objectives: To assay the incidence of listeriosis in our area from July 1998 to October 1999.
Methods: The samples were cultured in the habitual media. We isolated *L. monocytogenes* in 19 samples from 12 patients.
Results: The following panel shows the results in each paticnt.

Date	Sex	Age	Disease	Sample	Empirical treatment	Outcome	Underlying disease
7/98	M	72	Meningitis Encephalitis	CSF CSF,	V[4] + C[5] V + C +	Exitus	Arthritis
8/98	U	76	Bacteremia	Blood	A[6]	Favorable	Alcoholism
10/98	M	68	Arthritis	Synovial fluid	A	Favorable	NO
1/99	M	1	Meningitis	CSF GS[1], NS[2],	C + A	Favorable	Hepatic disease
3/99	F	NB	Meningitis	CSF	A + G[7]	Favorable	Newborn
4/99	M	87	Endoph-thalmitis	Vitreous humor	V + C	Enucleation	Prostatic tumor
4/99	M	47	Fever Encephalitis	Blood CSF	V + C	Exitus	Hepatic disease
5/99*	M	49	Bacteremia	Blood	C + V	Exitus	NO
5/99	M	65	Distres	Blood	NO V + C +	Exitus	Lung tumor
6/99	M	70	Meningitis	CSF	A	Exitus	Linfome
9/99	F	73	Headache	CSF Blood, BA[3]	A + G	Favorable	Hepatic disease
10/99	M	New-born	Infectión	GS, S	A + G	Favorable	Fever

1. Gastric secretions; 2. Neonatal surface; 3. Bronchial aspirate; 4. Vancomycin; 5 Cefotaxim; 6. Ampicillin; 7. Gentamycin.

Conclusions: 1. The incidence found in our area (12 cases/14 months/600000 inhabitants) is much higher than the one usually described. 2. Mortality in our serie goes up to 41.6%, being higher in those patients in which ampicilin was not used as empiric treatment. 3. Age and underlying disease should be mentionated as predisposing factors. Only in one of the cases* there were no predisposing factors found.

MoP320 Parasitic infections in children. A 6-year retrospective study

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Objectives: To present the main microbiological and epidemiological data of parasitic infections in children, during a 6-year period (1993–1999).
Methods: The examination for parasites was a routine procedure in children (aged 2 months - 14 years) with diarrhea and other symptoms from the gastrointestinal tract, eosinophilia, growth disorders etc. Macroscopic and microscopic examination was performed in 3175 stool specimens (direct wet mount, after concentration and permanently stained smears with various stains), 148 duodenal aspirates and 467 cellophane tape preparations on microscope slides for pinworms. Examination of sputum and other biological material was performed less frequently on special request.
Results: A total of 298 cases of parasitic infections were diagnosed. The responsible pathogens included: 140 Enterobius vermicularis, 125 Giardia lamblia, 22 Trichuris trichiura, 16 Hymenolepis nana, 13 Ascaris lumbricoides, 5 Entamoeba histolytica, 5 Entamoeba coli and 2 Echinococcus granulosus. Mixed infection of two or more parasites occurred in 24 cases (8%). The majority of parasitic infections were found in immigrants from developing countries (56%). They were more prevalent in girls (58%) and between the ages of 2 and 8 years. The annual incidence of infections did not alter significantly over the study period. Seventeen cases of parasitic infection speading between family members were recognized as well.
Conclusions: The parasitic infections in children in Greece are relatively common. Early diagnosis and treatment combined with appropriate preventive hygienic measures, especially in immigrants, are very important to avoid their increase and further spreading.

MoP321 Abnormal genital bacterial colonization and obstetric problems

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Objectives: Study the genital flora of women follow up at an obstetric service of Coimbra to establish if the presence of specific microorganisms is significantly associated with preterm birth, prelabour rupture of the membranes and spontaneous abortions.
Methods: Twenty-three women were investigated. Vaginal and urethral swabs were collected and microbiological assement included cultures for aerobic and anaerobic bacteria, yeasts, mycoplasmas and *Chlamydiae trachomatis*
Results: Among the women who gave birth preterm, the microorganisms isolated included both bacterial and genital-mycoplasmas (50%), both bacteria and *Chlamydiae trachomatis* (66.7%), *Chlamydiae trachomatis* alone (33.3%), *Gardnerella vaginalis* alone (16.7%) and 16.7% have premature rupture of the membranes associated only with the presence of *Chlamydiae trachomatis*.

The prevalence of Ureaplasma urealyticum was highest in women having spontaneous abortions (57.1%) compared to women giving birth at term (44.4%) and preterm (50%). Chlamydiae trachomatis was found in similar proportion in women who gave birth at term (44.4%) and in women who have spontaneous abortions (42.9%).

Incidence of mixed microorganisms was highest in women who have spontaneous abortions (57.1%) compared to women who gave birth at term (33.3%).
Conclusions: The hight incidence of *Chlamydiae trachomatis* and *Ureaplasma urealyticum* could play a role in obstretic problems; there were no significant difference between women who gave birth preterm and at term.

MoP322 Respiratory virus infections during a six year period in Northern Stockholm, Sweden

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Objectives: It has been stipulated that respiratory syncytial virus (RSV) is a more frequent cause of respiratory disease among the elderly than earlier believed. The diversity of respiratory viruses among patients mainly attending hospitals in the northern part of Stockholm was examined retrospectively.
Methods: From January 1993 until June 1999 6305 nasopharyngeal aspirates and throat swabs were analysed at our laboratory. Vires isolation as well as antigen detection (immunofluorescence) were performed on 4935 (78%) samples, antigen detection only on 874 (14%) and vires isolation only on 496 (8%). 1062 samples were from patients older than 64, and 3217 from patients younger than 6 years.
Results: In the total material we found 1136 influenza A (IA), 218 influenza B (IB), 997 RSV, 192 parainfluenza 1–3 (PIV), 119 adenovirus, 20 enterovirus, 71 herpes simplex type 1 and 2 (HSV), 6 cytomegalovirus and 6 measles virus infections. In samples from patients older than 64 we found 503 IA, 60 IB, 22 RSV, 12 PIV, 11 HSV and 1 CMV.
Conclusion: RSV is not common among the elderly.

MoP323 Changes in the prevalence of HCV genotypes 4. A three-year study in Calabria, Southern Italy

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Objectives: The aim of this study was to assess changes in the prevalence of Hepatitis C virus (HCV) genotypes by surveying population of chronic hepatitis C patients within an area of Southern Italy. We have previously observed, in a period of 18 months (January 1997–May 1998) an initial increase of the genotype 4 which appeared in 2.6% of patients versus 1.3% during 1996. Here we reported data on 702 HCV-RNA positive patients, collected from June 1998 until December 1999. Drug addiction, blood transfusion and sporadically acquired infections represented the risk factors.
Methods: HCV-RNA was detected in serum using two commercial hepatitis C RNA PCR assay (Amplicor Roche Diagnostic System, Italy, and AmpliSensor HCV, Nuclear Laser Medicine, Italy). PCR products were analyzed for genotyping using a reverse hybridization of the amplified product by a line probe assay (INNO LIPA HCV II, Innogenetics N.V., Belgium).

Results: Genotype 1b, the most prevalent isolate (58.1%) and genotype 2a/2c (24.8%) were associated with older age, confirming our previous study. Genotype 4, togheter with genotype 1a/1b (3.8%) represented the third genotype found in patients tested with a percentage of 3.7. On the contrary genotypes 1a and 3 showed a decreased prevalence. Lack of data from the rest of Italy does not allow a comparison with our results, however, while HCV seems to be associated with younger age, diffusion of genotype 4 in Calabria region is mostly associated to older age (76.9% of patients ranging from 45 to 82 years old).
Conclusions: We demonstrate an increased prevalence of HCV genotype 4 despite to lowering prevalence of other types in one restricted geographical area.

MoP324 Hepatitis B within the eradication project by vaccination and non A-B-C hepatitis - results of a two-year study in the Cluj-Napoca Medical School Hospital

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Objectives: To establish the epidemiological pattern of acute viral hepatitis (VH) in a tertiary care facility, after introducing the hepatitis B vaccination (1995) and confirmatory serological tests for acute viral hepatitis A, B, C (1998).
Methods: We retrospectively studied all acute viral hepatitis admitted in the Cluj-Napoca tertiary care center during 1998–99. We designed a database using the medical records comprising: demographic data, premorbid conditions, possible exposures, bilirubin, SGOT/SGPT, other biochemical tests, main serological markers for acute infection (IgM anti-HAV, IgM anti-HBc, third generation HCV EIA). EPI6 software was used for statistical analysis.
Results: 1999 represented an epidemic year for hepatitis A (440 cases, 76%). Hepatitis B was in statistically significant decrease (12%, p- .000) with only 1 case in children under 5 years, the infants' vaccine coverage being > 90%. Hepatitis C was also in significant decrease (8%, p- .003) and less then 5% represented non A-B-C hepatitis which occurred in adults or elderly with a good socio-economic status and without travel exposures. Transient increased blood sugar levels were found in the elderly cases of non A-B-C VH. For all VH case-fatality ratio was 0.57% occurring in adults under 40 years.
Conclusions: The eradication project of hepatitis B demonstrate very good results with almost no cases in children, under a good notification of cases (mandatory hospitalization for all VH). Hepatitis C is also decreasing due to a better control of nosocomial exposures. The stored sera should be tested for HEV, which seem to be endemic in Romania.

MoP325 Prophylaxis of rabies in Lithuania in the period of 1989–1998

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Objective: The analysis of the epidemiological situation and imunoprophylaxis of Rabies.
Methods: The analysis of Rabies prevalence among people and animals and the vaccinacy level in Lithuania.
Results: During the period of 1989–1998 there were registered 1668 cases of animal Rabies in Lithuania, including 1117 cases among domestic animals and 551 cases among wild animals. The cases of Rabies among cattle (687 cases), dogs (207 cases) and foxes (308 cases) prevailed. The number of cases of Rabies among animals is continuously increasing every year (in 1989 - 105; in 1998 - 226 cases). Up to 1997 more than 2000 people (average 2341 persons) took medical advice because of being bitten all over by different animals and about 29.6% of the were vaccinated. In 1998 the number of bitten people increased up to the 8754 cases. The vaccinacy level reached 50.8%. The vaccination is free in Lithuania and it is carried out by the specialists of the appropriate doctors' surgeries and also by the doctors' of the reception sections of the hospitals. In the period of 1989–1998 there were registered 4 cases of human Rabies in Lithuania. Every year about 25 000 domestic animals are vaccinated and about 200 000 (20–25 km^2) baits were poured out over the forests in order to vaccinate foxes.
Conclusions: As the prevalence of animals Rabies is continuously increasing, it is obligatory to vaccinate domestic animals as well as wild animals. It is necessary to increase the level of vaccination and vaccination must be compulsory. In order to prevent the cases of human Rabies a pre-contactic vaccination among the people belonging to the risk groups must be carried out.

MoP326 Prevailing subtype in patients with acute hepatitis C virus infection

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Objectives: The aim of this study is to show the predominant subtype of HCV in Thracia region in Bulgaria.
Methods: Fifty patients with diagnosis of acute viral hepatitis C were serotyped by Murex HCV Serotyping 1–6 Assay. In six months period after discharge every case was followed for five years. In 20 of all patients two biopsies were made in this period.
Results: 42 cases were with subtype 1a (84%); 2 were with 1a + 1b (4%) and 6 with 1b (12%).
Conclusions: The prevalent subtype of HCV infection in Thracia region is subtype 1a (84% in our study) which differs in comparison with Western Europe where the prevailing subtype is 1b.

MoP327 Prevalence of HBsAg, Anti-HBs and Anti-HCV in outpatients of medical department in a university hospital

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Objectives: To investigate the prevalence of HBsAg, Anti-HBs and Anti-HCV positivity among patients who applied for different reasons to the outpatient clinic of the department of internal medicine of a university hospital.
Methods: The frequencies of HBsAg, Anti-HBs and Anti-HCV positivity were determined in 1000 randomly selected patients. The patients were also evaluated in regard to present and past medical histories, family histories, physical examination and routine laboratory examinations.
Results: The prevalence ofHBsAg was 9.6% and the prevalence of Anti-HBs was 24.5%. With regard to HBsAg positivity, there was a significant difference ($p < 0.01$) between the group of 717 patients who carry some kind a risk for HBV and the group of 283 patients with no known risk. It was observed that being a relative of a HBV carrier formed the highest risk factor for HBV infection. Anti-HCV positivity was determined to be 2.1% in population examined.
Conclusion: Our findings are in compliance with some data in previous studies carried out in this countr.

MoP328 EU antibiotic resistance monitoring in bacteria of animal origin

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Objectives: Emergence and spread of resistance to antibiotics has been a subject of main concern in the last decades and the prudent use of antimicrobials, notably in veterinary medicine and agriculture has been widely discussed. Many scientific committees discussed recently the possible issues and agreed that the development of resistance in humans could be correlated to its spread in animals and that a surveillance should be set up in bacteria of animal origin. This communication aims at presenting the minimum epidemiological and microbiological requirements for a monitoring of antimicrobial resistance in bacteria of animal origin.
Results: After analysing the monitoring systems in 13 European countries, a common structure of surveillance was proposed. Regardless from the methodology used for susceptibility testing (dilution or diffusion), the group agreed that storage of quantitative raw data was necessary either as MIC or inhibition diameters depending on the bacterial species monitored. These species were categorised in 3 groups, veterinary pathogens, zoonotic agents, and indicator bacteria. For each of these 3 groups, the bacterial species

to be monitored, groups of animals, sampling Isolation and susceptibility testing strategies and finally data collected were defined.
Conclusion: Collecting these data through an harmonised method at an European level aims at better controlling new resistance emergence and spread through the analysis of comparable data, providing European reports on resistance trends. These data will be useful to develop guidelines for prudent use of antimicrobials in veterinary medicine and could be used by practitioners to help them in their prescriptions.

MoP329 AFLP typing of *Salmonella* strains

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Objectives: The AFLP technique has been evaluated to characterise 42 Salmonella strains isolated from clinical and environmental samples within 12 different serotypes.
Methods: 10 μl of genomic DNA were digested at 37°C with 20 units of HindIII in a final volume of 20 μl. Ligation reaction was developed with 0.2 μl of ADH1 and ADH2 adapters, 1 unit of T4 ligase and 5 μl of the pre-digested DNA, at 37°C for 3–4 h. Ligated DNA was heated at 80°C for 10 min. and a 5 μl aliquote was amplified with the primer 5'-GGTATGC-GACCAGAGCTTC-3'. Amplified fragments were separated by electrophoresis on 2.5% agarose gel in TAE buffer. DNA bands patterns were analysed with the image analysis software TDI Program, and numerical correlation was determined with NTSYS program.
Results: Each AFLP type presents a unique banding pattern. With the exceptions of S. bredeney and S. ohio serotypes, strains with the same serotype are included in the same AFLP type, or share a high number of common bands. Each serogroup of clinical isolates present the same AFLP type, and all of them share two common bands with the rest of the strains analysed in this study.
Conclusions: results show the usefulness of AFLP technique to serotype-specific even to strain-specific identification of Salmonella. Clinical AFLP types are serogroup-specific and they are different from strains isolated from environmental sources.

MoP330 Shift of serotype in one and the same genotype – A result of phenotypic selection?

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Objectives: Identification of sources and reservoirs for strain-specific infectious *Pseudomonas aeruginosa* in occupational saturation diving systems.
Methods: Through a 14 year consecutive infection and environment control programme in diving systems in the North Sea, a microbial collection including *P. aeruginosa*, the main infectious microbe, is available. Epidemiological analyses have consecutively been done by use of biotyping, serotyping and a novel "ABF-marker". Retrospective genetic analyses by use of restriction enzyme fragmentation and PFGE and repeated serotyping have been performed on parts of this strain collection.
Results: One hundred and eighty one *P. aeruginosa* infectious isolates from divers skin infections and three hundred and ninety environmental isolates of the same microbe have been analysed. A few serotypes dominate of which serotype O11 has been dominant over the whole period. A total of 104 genotypes have been identified, some of which detected over many years. In nine genotypes, a shift in serotype has been demonstrated during the observation period. Among these are five of the frequent infectious genotypes. Shift of serotype has never been seen upon repeated serotyping nor does the shift reflect closely related serotypes.
Conclusion: Both phenotyping and genotyping indicate selection of *P. aeruginosa* from skin infections in divers. We therefore conclude that shift in serotype could be a result of phenotypic selection in this unique environment.

MoP332 PFGE, AFLP and MAb subtyping of Legionella pneumophila sg 1

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Objectives: To compare Pulsed Field Gel Electrophoresis (PFGE), Amplified Fragment Length Polymorphism (AFLP) and subtyping by monoclonal antibodies (MAb), in an investigation of an outbreak, caused by Legionella pneumophila serogroup (sg) 1, comprising 14 patients at a university hospital.
Methods: Six patient and 10 environmental isolates from the hospital together with 20 other, mostly patient isolates, that were unrelated to the outbreak, were analysed. All isolates were L. pneumophila sg 1. PFGE was performed subsequent to macrorestriction by SfiI. AFLP fragments were generated by PstI digestion and ligated to specific primers which could be used as templates for PCR. All strains were subtyped using MAb belonging to the Dresden panel.
Results: All patient and environmental isolates from the outbreak hospital were of the same genotype in both PFGE and AFLP. This genotype was distinctly different from those of other strains, including a cluster in a different part of the country. The MAb subtype was Knoxville except for one isolate, that was OLDA/Oxford. Different LPS phenons (MAb subtypes) belonging to the same genotype were also demonstrated in two other clusters.
Conclusions: Both PFGE and AFLP discriminated the outbreak strain clearly from other strains. MAb subtypes are less discriminatory but might be of value initially during an outbreak investigation.

P:14/4 – Emerging infections

MoP333 Epidemiology of haemorrhagic fever with renal syndrome in West Georgia

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The investigations on the epidemiology of *Haemorrhagic fever with renal syndrome (HFRS)* in West Georgia were conducted. In different landscape-climat zones natural foci of *HFRS* differing in ecologic conditions and the activity of epizootic process have been revealed.

Clinical, virologic and serologic (immunofluorescent antibody. haemagglutination-inhibition and immunoassay tests) examinations of patients, immune layer of population and small mammals.

Haemorrhagic fever with renal syndrome was diagnosed 61 patients. Human contamination with the *HFRS* virus was mostly conducted by airborne way. Among patients with *Haemorrhagic fever with renal syndrome* the morbidity rate was the highest in age groups from 30 to 39 years (46.0%). *Haemorrhagic fever with renal syndrome* characterized by marred seasonal prevalence. 90.1 per cent of cases are registered at the end of spring and in early autumn. Immune layer of population of *HFRS virus* was 1.8 per cent. The *HFRS virus* was detected in small mammals of 5 different species Rattus rattus, Rattus norvegicus, Mus musculus, Apodemus silvaticus and Crocidura longicaudata.

Thus, the circulation of *Haemorrhagic fever with renal syndrome virus* in West Georgia has been demonstrated.

MoP334 Characteristics of *Borrelia burgdorferi* sensu lato strains isolated from patients in Poland

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Objective: To differentiate 25 *Borrelia burgdorferi* sensu lato strains isolated from patients with Lyme borreliosis.
Methods: Blood, synovial and cerobrospinal fluids collected from patients with symptoms of Lyme borreliosis were cultured in L-925 cell line for 10 days. Isolated bacterial DNA was amplified by PCR with two pairs of primers: for 16S RNA and rrf(5S)-rrl(23S) gene fragments. Primers for 16S RNA gene were used to detect *B. burgdorferi* sensu lato DNA. Amplification products of second pair of primers were digested with endonuclease *MseI*. Digestion products were run in agarose gel electrophoresis.

Level of specific antibodies in tested materials was measured by ELISA with recombinant antigens (BIOMEDICA, Austria).